



Behavior of a Discrete SIR Epidemic Model

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Abstract: In this paper, we propose a discrete-time SIR epidemic model described by difference equations. The basic reproductive number R_0 of a discrete SIR epidemic model is computed and the dynamical behavior of the model is studied. The stability the disease free equilibrium and the endemic equilibrium are demonstrated. Numerical simulations are performed to illustrate the theoretical results.

Keywords: Epidemic Model, difference equations, stability.

I. Introduction

Infections and infectious diseases are a great burden on many societies, including the countries. An epidemic may be described as a sudden outbreak of a disease that infects a substantial portion of the population in a region before it disappears. In the nineteenth century, recurrent waves of cholera killed millions in India. The influenza epidemic of 1918-1919 killed at least 20 million people overall, more than half a million in the United States. Epidemics of infectious diseases have been documented throughout history. Mathematical models provide an explicit framework within which to develop and communicate an understanding of infectious disease transmission dynamics. The earliest account of mathematical modeling of spread of disease was carried out in 1766 by Daniel Bernoulli. The SIR model is a simple model, due to Kermack and McKendrick, of an epidemic of an infectious disease in a population, [3]. In the theoretical studies of epidemic dynamical models, there are two kinds of mathematical models: the continuous-time models described by differential equations, and the discrete-time models described by difference equations. Analysis of steady states of the model and the stability for the epidemic model is of a great importance as it can help our society and direct us to determine and forecast the development trend of infection. The solution results can be used to describe the spread characteristics of infectious diseases, predict the status of the infection and evaluate the efficiency of the control strategies.

II. Formulation of Model

The host population is divided into three epidemiological classes: the susceptibles S , the infectives I , and the removed/recovered. Few authors studied discrete epidemic models [2, 4, 6] where as there exists a vast literature on continuous epidemic models [1, 5]. In this section, we analyze the following discrete SIR epidemic model.

$$\begin{aligned} S(n+1) &= b - \beta S(n)I(n) + (1 - \mu)S(n) \\ I(n+1) &= \beta S(n)I(n) + [1 - (\gamma + \mu + \alpha)]I(n) \\ R(n+1) &= \gamma I(n) + (1 - \mu)R(n) \end{aligned}$$

where $b, \beta, \mu, \gamma, \alpha > 0$ and the initial conditions are $S(0) > 0, I(0) > 0, R(0) > 0$. The parameters have the following meaning: b is the birth rate, μ is the death rate, β is the average number of contacts per infective per day, γ is the recovery rate, and α is the death rate of infectives caused by the disease. The system (1) always has a disease-free equilibrium $E_0 = (\frac{b}{\mu}, 0, 0)$ and an endemic equilibrium $E_1 = [\frac{A}{\beta}, \frac{b}{A} - \frac{\mu}{\beta}, \gamma(\frac{b}{\mu A} - \frac{1}{\beta})]$, where $A = (\gamma + \mu + \alpha)$. E_0 is called the disease free equilibrium since I and R classes are empty.

III. Dynamic Behavior of the Model and Numerical Simulations

This section deals with the stability of equilibria. By mathematical analysis, we derive a threshold value R_0 and prove that the values of R_0 determine the dynamics of system. An important technique for analyzing nonlinear systems qualitatively is the analysis of the behavior of the solutions near equilibrium points using linearization. For the discrete time model, stability of the equilibrium solution requires the dominant eigenvalue to have magnitude less than one. For the system described by equations (1), this reduces to requiring all roots of the following equation to lie in the unit circle [6]. The local stability analysis of the model can be carried out by computing the Jacobian matrix corresponding to each equilibrium point. We first determine the stability of the system. The Jacobian matrix of system (1) is

$$J(S, I, R) = \begin{bmatrix} -\beta I + (1 - \mu) & -\beta S & 0 \\ \beta I & \beta S + 1 - A & 0 \\ 0 & \gamma & 1 - \mu \end{bmatrix}$$

A. Disease Free Equilibrium. At the disease-free equilibrium, the matrix of the linearization is given by

$$J(E_0) = \begin{bmatrix} (1 - \mu) & \frac{-\beta b}{\mu} & 0 \\ 0 & \frac{\beta b}{\mu} + 1 - A & 0 \\ 0 & \gamma & 1 - \mu \end{bmatrix}$$

The eigen values of the matrix $J(E_0)$ are $\lambda_1 = \lambda_2 = 1 - \mu$ and $\lambda_3 = \frac{\beta b}{\mu} - [1 - A]$. The basic reproductive number, R_0 , is fundamental in the study of epidemiological models. Here the basic reproductive number $R_0 = \frac{\beta b}{\mu A} < 1$, where $A = (\gamma + \mu + \alpha)$. The epidemic spreads when $R_0 > 1$ and dies out when $R_0 < 1$. If $R_0 < 1$, the disease-free equilibrium E_0 is stable.

Example 1. We choose the parameter values $b = 0.05$; $\beta = 1.195$; $\mu = 0.18$; $\gamma = 0.29$; $\alpha = 0.09$ and the initial condition $(S, I, R) = (0.85, 0.15, 0.0)$. Here $R_0 = \frac{\beta b}{\mu} = 0.5927 < 1$; so the equilibrium point E_0 is globally stable, see fig - 1.

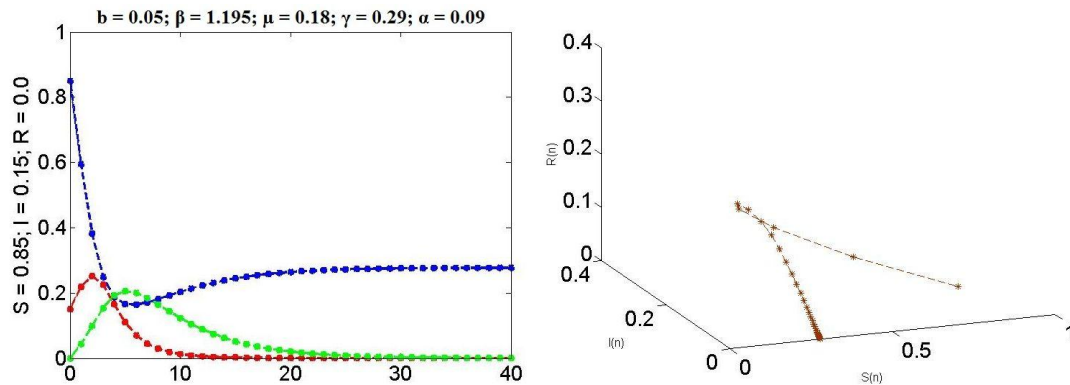


Figure 1. Time plot and Phase diagram for the system (1) with $R_0 < 1$

Thus the disease free equilibrium of (1) is asymptotically stable when $R < 1$. In the following figure, the effect of the parameter β on the disease dynamics (infection) is demonstrated.

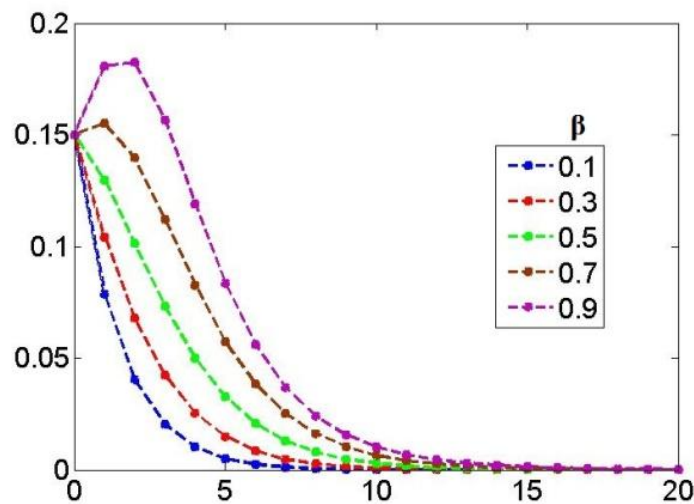


Figure 2. Variation of β

Example 2. Choose the parameter $b = 0.13; \beta = 1.12; \mu = 0.13; \gamma = 0.09; \alpha = 0.9$ and the initial condition $(S, I, R) = (0.85, 0.15, 0.0)$. Here $R_0 = \frac{\beta b}{\mu} = 1$; so the equilibrium point E_0 is globally stable, see fig - 3.

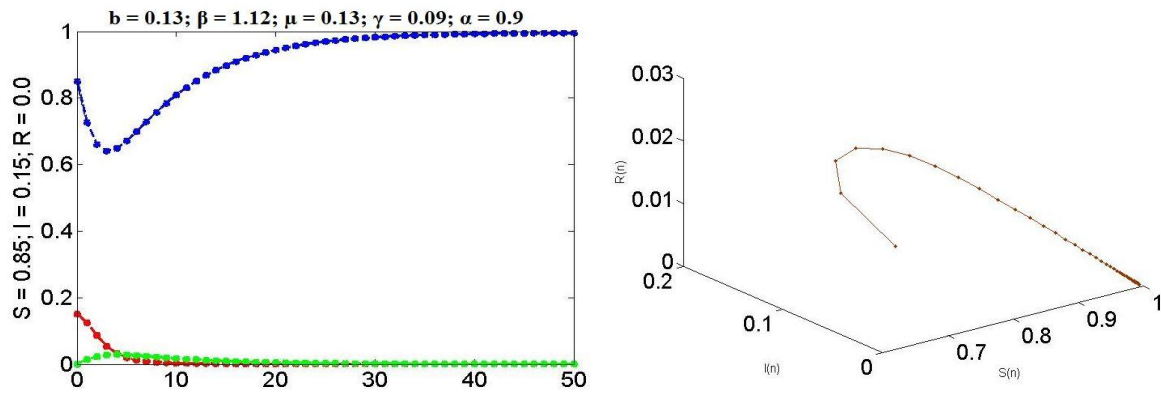


Figure 3. Time plot and Phase diagram for the system (1) with $R_0 = 1$

3.2. Endemic Equilibrium. The linearization matrix of (1) at the positive equilibrium E_1 is,

$$J(E_1) = \begin{bmatrix} 1 - \frac{\beta b}{A} & -A & 0 \\ \frac{\beta b}{A} - \mu & 1 & 0 \\ 0 & \gamma & 1 - \mu \end{bmatrix}$$

The eigen values of the matrix $J(E_1)$ are $\lambda_1 = 1 - \mu$ and $\lambda_{2,3} = 1 - \frac{\beta b}{2A} \pm \frac{1}{2A} \sqrt{4\mu A^3 - 4A^2\beta b + \beta^2 b^2}$, where $A = (\gamma + \mu + \alpha)$. If $R_0 > 1$ the endemic equilibrium E_1 is stable.

Example 3. Choose the parameter $b = 0.43; \beta = 1.69; \mu = 0.1; \gamma = 0.1933; \alpha = 0.8$ and the initial condition $(S, I, R) = (0.5, 0.6, 0.4)$. Here $R_0 = 6.6468 > 1$; so the equilibrium point E_1 is asymptotically stable, see fig - 4. When $R_0 > 1$, the average number of a new infection by an infected individual is more than one. Hence the disease may keep persistent in the population.

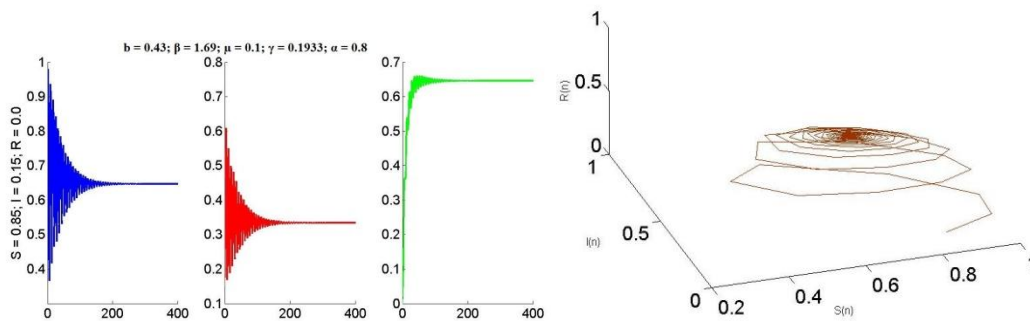


Figure 4. Time plot and Phase diagram for the system (1) with $R_0 > 1$

The discrete SIR model considered in this paper is simple, but it exhibits rich and complicated dynamical behavior. The analytical findings are confirmed with numerical simulations.

IV. References

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